

Wed Jul 13 13:49:43 2005

us-09-788-074-4.rmpn

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 17:41:25 ; Search time 1316.5 Seconds  
(without alignments)  
2368.781 Million cell updates/sec

Title: US-09-788-074-4

Perfect score: 662  
Sequence: 1 accgcgcgacgcagaccctc.....taataaatgtttgtgtct 662

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16258531 seqs, 2355356875 residues

Total number of hits satisfying chosen parameters: 32517062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Pending\_Patents\_NA\_New:\*  
1: /cgn2\_6/prodata/2/pna/PCT\_NEW\_COMB.seq:\*  
2: /cgn2\_6/prodata/2/pna/PCT\_NEW\_COMB.seq2:\*  
3: /cgn2\_6/prodata/2/pna/US06\_NEW\_COMB.seq:\*  
4: /cgn2\_6/prodata/2/pna/US07\_NEW\_COMB.seq:\*  
5: /cgn2\_6/prodata/2/pna/US08\_NEW\_COMB.seq:\*  
6: /cgn2\_6/prodata/2/pna/US09\_NEW\_COMB.seq:\*  
7: /cgn2\_6/prodata/2/pna/US10\_NEW\_COMB.seq:\*  
8: /cgn2\_6/prodata/2/pna/US10\_NEW\_COMB.seq2:\*  
9: /cgn2\_6/prodata/2/pna/US10\_NEW\_COMB.seq3:\*  
10: /cgn2\_6/prodata/2/pna/US10\_NEW\_COMB.seq4:\*  
11: /cgn2\_6/prodata/2/pna/US10\_NEW\_COMB.seq5:\*  
12: /cgn2\_6/prodata/2/pna/US10\_NEW\_COMB.seq6:\*  
13: /cgn2\_6/prodata/2/pna/US11\_NEW\_COMB.seq:\*  
14: /cgn2\_6/prodata/2/pna/US11\_NEW\_COMB.seq2:\*  
15: /cgn2\_6/prodata/2/pna/US11\_NEW\_COMB.seq3:\*  
16: /cgn2\_6/prodata/2/pna/US11\_NEW\_COMB.seq4:\*  
17: /cgn2\_6/prodata/2/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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US-09-788-074-4.rupm

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 18:01:50 ; Search time 3043.97 Seconds  
(without alignments)  
8878.154 Million cell updates/sec

Title: US-09-788-074-4

Perfect score: 662

Sequence: 1 accgcgcgcgcgcaccctc.....caataaatgtgttgct 662

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext: 1.0

Searched: 4554873 seqs, 2041521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :